

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/591,628
Source: IFWP
Date Processed by STIC: 9/13/06

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IFWP

RAW SEQUENCE LISTING

DATE: 09/13/2006

PATENT APPLICATION: US/10/591,628

TIME: 11:11:47

Input Set : A:\A0852.70000US01 seq.txt

Output Set: N:\CRF4\09132006\J591628.raw

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3 <110> APPLICANT: Adra, Chaker
5 <120> TITLE OF INVENTION: GRANULOCYTE SUBTYPE-SELECTIVE RECEPTORS AND ION CHANNELS AND
USES
6     THEREOF
8 <130> FILE REFERENCE: A0852.70000WO00
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/591,628
11 <141> CURRENT FILING DATE: 2006-09-05
13 <150> PRIOR APPLICATION NUMBER: PCT/US2005/007519
14 <151> PRIOR FILING DATE: 2005-03-03
16 <150> PRIOR APPLICATION NUMBER: 60/549,865
17 <151> PRIOR FILING DATE: 2004-03-03
19 <160> NUMBER OF SEQ ID NOS: 31
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 557
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
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31 ctgtagtgtc aagttctttc aaacttaaaa ttttaacccc agaggatttt cgctgaataa      120
33 atgagaattg gctctatttc ttctacttct ggatagcccg agtaaaaata ctaataattt      180
35 ctagatttta gtggggaact acaattatta ggacccatgg atattgctgc agttcaaata      240
37 caatacagta attacaaaat atagaccatc tctttacaaa tacaaattat agtatattac      300
39 aagtcagtga cagtaaatct ataattttaa acaaaactagt gtatctaagt ttacctgggt      360
41 gcgagtgcat tattattcca gtttacagtt gcccttagcg tgacagtcag aaaccgacca      420
43 tcggagtgat attctcttat gtaaaactggc gtcacatcac agaaaacctt atttatgagg      480
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47 tcagaacagc taaacag
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51 <211> LENGTH: 1613
52 <212> TYPE: DNA
53 <213> ORGANISM: Homo sapiens
55 <220> FEATURE:
56 <221> NAME/KEY: CDS
57 <222> LOCATION: (71)..(1198)
59 <400> SEQUENCE: 2
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62 gagcctggca atg gat gcc att cac atc ggc atg tcc agc acc ccc ctg      109
63     Met Asp Ala Ile His Ile Gly Met Ser Ser Thr Pro Leu
64     1             5             10
66 gtg aag cac act gct ggg gct ggg ctc aag gcc aac aga ccc cgc gtc      157
67 Val Lys His Thr Ala Gly Ala Gly Leu Lys Ala Asn Arg Pro Arg Val
68     15             20             25
70 atg tcc aag agt ggg cac agc aac gtg aga att gac aaa gtg gat ggc      205

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74 ata tac cta ctc tac ctg caa gac ctg tgg acc aca gtt atc gac atg      253
75 Ile Tyr Leu Leu Tyr Leu Gln Asp Leu Trp Thr Thr Val Ile Asp Met
76          50          55          60
78 aag tgg aga tac aaa ctc acc ctg ttc gct gcc act ttt gtg atg acc      301
79 Lys Trp Arg Tyr Lys Leu Thr Leu Phe Ala Ala Thr Phe Val Met Thr
80          65          70          75
82 tgg ttc ctt ttt gga gtc atc tac tat gcc atc gcg ttt att cat ggg      349
83 Trp Phe Leu Phe Gly Val Ile Tyr Tyr Ala Ile Ala Phe Ile His Gly
84          80          85          90
86 gac tta gaa ccc gat gag ccc att tca aat cat acc ccc tgc atc atg      397
87 Asp Leu Glu Pro Asp Glu Pro Ile Ser Asn His Thr Pro Cys Ile Met
88          95          100          105
90 aaa gtg gac tct ctc act ggg gcg ttt ctc ttt tcc ctg gaa tcc cag      445
91 Lys Val Asp Ser Leu Thr Gly Ala Phe Leu Phe Ser Leu Glu Ser Gln
92 110          115          120          125
94 aca acc att ggc tat gga gtc cgt tcc atc aca gag gaa tgt cct cat      493
95 Thr Thr Ile Gly Tyr Gly Val Arg Ser Ile Thr Glu Glu Cys Pro His
96          130          135          140
98 gcc atc ttc ctg ttg gtt gct cag ttg gtc atc acg acc ttg att gag      541
99 Ala Ile Phe Leu Leu Val Ala Gln Leu Val Ile Thr Thr Leu Ile Glu
100          145          150          155
102 atc ttc atc acc gga acc ttc ctg gcc aaa atc gcc aga ccc aaa aag      589
103 Ile Phe Ile Thr Gly Thr Phe Leu Ala Lys Ile Ala Arg Pro Lys Lys
104          160          165          170
106 cgg gct gag acc atc aag ttc agc cac tgt gca gtc atc acc aag cag      637
107 Arg Ala Glu Thr Ile Lys Phe Ser His Cys Ala Val Ile Thr Lys Gln
108          175          180          185
110 aat ggg aag ctg tgc ttg gtg att cag gta gcc aat atg agg aag agc      685
111 Asn Gly Lys Leu Cys Leu Val Ile Gln Val Ala Asn Met Arg Lys Ser
112 190          195          200          205
114 ctc ttg att cag tgc cag ctc tct ggc aag ctc ctg cag acc cac gtc      733
115 Leu Leu Ile Gln Cys Gln Leu Ser Gly Lys Leu Leu Gln Thr His Val
116          210          215          220
118 acc aag gag ggg gag cgg att ctc ctc aac caa gcc act gtc aaa ttc      781
119 Thr Lys Glu Gly Glu Arg Ile Leu Leu Asn Gln Ala Thr Val Lys Phe
120          225          230          235
122 cac gtg gac tcc tcc tct gag agc ccc ttc ctc att ctg ccc atg aca      829
123 His Val Asp Ser Ser Ser Glu Ser Pro Phe Leu Ile Leu Pro Met Thr
124          240          245          250
125 ttc tac cat gtg ctg gat gag acg agc ccc ctg aga gac ctc aca ccc      877
126 Phe Tyr His Val Leu Asp Glu Thr Ser Pro Leu Arg Asp Leu Thr Pro
127          255          260          265
129 caa aac cta aag gag aag gag ttt gag ctt gtg gtc ctc ctc aat gcc      925
130 Gln Asn Leu Lys Glu Lys Glu Phe Glu Leu Val Val Leu Leu Asn Ala
131 270          275          280          285
133 act gtg gaa tcc acc agc gct gtc tgc cag agc cga aca tct tat atc      973
134 Thr Val Glu Ser Thr Ser Ala Val Cys Gln Ser Arg Thr Ser Tyr Ile

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135          290          295          300
137 cca gag gaa atc tac tgg ggt ttt gag ttt gtg cct gtg gta tct ctc      1021
138 Pro Glu Glu Ile Tyr Trp Gly Phe Glu Phe Val Pro Val Val Ser Leu
139          305          310          315
141 tcc aaa aat gga aaa tat gtg gct gat ttc agt cag ttt gaa cag att      1069
142 Ser Lys Asn Gly Lys Tyr Val Ala Asp Phe Ser Gln Phe Glu Gln Ile
143          320          325          330
145 cgg aaa agc cca gat tgc aca ttt tac tgt gca gat tct gag aaa cag      1117
146 Arg Lys Ser Pro Asp Cys Thr Phe Tyr Cys Ala Asp Ser Glu Lys Gln
147          335          340          345
149 caa ctc gag gag aag tac agg cag gag gat cag agg gaa aga gaa ctg      1165
150 Gln Leu Glu Glu Lys Tyr Arg Gln Glu Asp Gln Arg Glu Arg Glu Leu
151 350          355          360          365
153 agg aca ctt tta tta caa cag agc aat gtc tga tcacaggggc gccatccagg      1218
154 Arg Thr Leu Leu Gln Gln Ser Asn Val
155          370          375
157 ttttaaccctg caagctgttt ccacatcaga actcccttca aacacaaaga ttgctgtgaa      1278
159 aacgaaaatg tgtagacgca ctctcaaaaa ctgcacggac atacaaaatc aatcttttcc      1338
161 tttgatcttg tggctaaacc agcatttctg tgtttgagag atttctgtt aggtgcttcg      1398
163 tctgaaagtg aactctcata attcaaattg tataaaataa agctacattt ctaagagctt      1458
165 ggtgtagggc aattggaata atgtcctgtt agataaacag acatttagca atgctgacat      1518
167 taaaaggaaa tgtatttcta tacaagatta ttagctgtaa tacaagatat ttatttaacc      1578
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174 <212> TYPE: PRT
175 <213> ORGANISM: Homo sapiens
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183 Thr Ala Gly Ala Gly Leu Lys Ala Asn Arg Pro Arg Val Met Ser Lys
184          20          25          30
187 Ser Gly His Ser Asn Val Arg Ile Asp Lys Val Asp Gly Ile Tyr Leu
188          35          40          45
191 Leu Tyr Leu Gln Asp Leu Trp Thr Thr Val Ile Asp Met Lys Trp Arg
192          50          55          60
195 Tyr Lys Leu Thr Leu Phe Ala Ala Thr Phe Val Met Thr Trp Phe Leu
196 65          70          75          80
199 Phe Gly Val Ile Tyr Tyr Ala Ile Ala Phe Ile His Gly Asp Leu Glu
200          85          90          95
203 Pro Asp Glu Pro Ile Ser Asn His Thr Pro Cys Ile Met Lys Val Asp
204          100          105          110
207 Ser Leu Thr Gly Ala Phe Leu Phe Ser Leu Glu Ser Gln Thr Thr Ile
208          115          120          125
211 Gly Tyr Gly Val Arg Ser Ile Thr Glu Glu Cys Pro His Ala Ile Phe
212          130          135          140
215 Leu Leu Val Ala Gln Leu Val Ile Thr Thr Leu Ile Glu Ile Phe Ile
216 145          150          155          160
219 Thr Gly Thr Phe Leu Ala Lys Ile Ala Arg Pro Lys Lys Arg Ala Glu

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220          165          170          175
223 Thr Ile Lys Phe Ser His Cys Ala Val Ile Thr Lys Gln Asn Gly Lys
224          180          185          190
227 Leu Cys Leu Val Ile Gln Val Ala Asn Met Arg Lys Ser Leu Leu Ile
228          195          200          205
231 Gln Cys Gln Leu Ser Gly Lys Leu Leu Gln Thr His Val Thr Lys Glu
232          210          215          220
235 Gly Glu Arg Ile Leu Leu Asn Gln Ala Thr Val Lys Phe His Val Asp
236 225          230          235          240
239 Ser Ser Ser Glu Ser Pro Phe Leu Ile Leu Pro Met Thr Phe Tyr His
240          245          250          255
243 Val Leu Asp Glu Thr Ser Pro Leu Arg Asp Leu Thr Pro Gln Asn Leu
244          260          265          270
247 Lys Glu Lys Glu Phe Glu Leu Val Leu Leu Asn Ala Thr Val Glu
248          275          280          285
249 Ser Thr Ser Ala Val Cys Gln Ser Arg Thr Ser Tyr Ile Pro Glu Glu
250          290          295          300
253 Ile Tyr Trp Gly Phe Glu Phe Val Pro Val Val Ser Leu Ser Lys Asn
254 305          310          315          320
257 Gly Lys Tyr Val Ala Asp Phe Ser Gln Phe Glu Gln Ile Arg Lys Ser
258          325          330          335
261 Pro Asp Cys Thr Phe Tyr Cys Ala Asp Ser Glu Lys Gln Gln Leu Glu
262          340          345          350
265 Glu Lys Tyr Arg Gln Glu Asp Gln Arg Glu Arg Glu Leu Arg Thr Leu
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270          370          375
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274 <211> LENGTH: 5397
275 <212> TYPE: DNA
276 <213> ORGANISM: Homo sapiens
278 <220> FEATURE:
279 <221> NAME/KEY: CDS
280 <222> LOCATION: (384)..(1667)
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287 acccccccact tccactccat gtcccatgc tctgcgcca gcaacaggac atgttctctg      180
289 gatgtcagct gagtcattaa agtaactctg catgtcagta gacagacctt ggtagaacca      240
291 caaggctccc agagacaccc atctctcctc atttttttgg tgtgtgtgtc ttcaccgaac      300
293 attcaaaact gtttctccaa agcgttttgc aaaaactcag actgttttcc aaagcagaag      360
295 cactggagtc cccagcagaa gcg atg ggc agt gtg cga acc aac cgc tac agc      413
296          Met Gly Ser Val Arg Thr Asn Arg Tyr Ser
297          1          5          10
299 atc gtc tct tca gaa gaa gac ggt atg aag ttg gcc acc atg gca gtt      461
300 Ile Val Ser Ser Glu Glu Asp Gly Met Lys Leu Ala Thr Met Ala Val
301          15          20          25
303 gca aat ggc ttt ggg aac ggg aag agt aaa gtc cac acc cga caa cag      509
304 Ala Asn Gly Phe Gly Asn Gly Lys Ser Lys Val His Thr Arg Gln Gln

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307 tgc agg agc cgc ttt gtg aag aaa gat ggc cac tgt aat gtt cag ttc				557
308 Cys Arg Ser Arg Phe Val Lys Lys Asp Gly His Cys Asn Val Gln Phe				
309 45 50 55				
311 atc aat gtg ggt gag aag ggg caa cgg tac ctc gca gac atc ttc acc				605
312 Ile Asn Val Gly Glu Lys Gly Gln Arg Tyr Leu Ala Asp Ile Phe Thr				
313 60 65 70				
315 acg tgt gtg gac att cgc tgg cgg tgg atg ctg gtt atc ttc tgc ctg				653
316 Thr Cys Val Asp Ile Arg Trp Arg Trp Met Leu Val Ile Phe Cys Leu				
317 75 80 85 90				
319 gct ttc gtc ctg tca tgg ctg ttt ttt ggc tgt gtg ttt tgg ttg ata				701
320 Ala Phe Val Leu Ser Trp Leu Phe Phe Gly Cys Val Phe Trp Leu Ile				
321 95 100 105				
323 gct ctg ctc cat ggg gac ctg gat gca tcc aaa gag ggc aaa gct tgt				749
324 Ala Leu Leu His Gly Asp Leu Asp Ala Ser Lys Glu Gly Lys Ala Cys				
325 110 115 120				
327 gtg tcc gag gtc aac agc ttc acg gct gcc ttc ctc ttc tcc att gag				797
328 Val Ser Glu Val Asn Ser Phe Thr Ala Ala Phe Leu Phe Ser Ile Glu				
329 125 130 135				
331 acc cag aca acc ata ggc tat ggt ttc aga tgt gtc acg gat gaa tgc				845
332 Thr Gln Thr Thr Ile Gly Tyr Gly Phe Arg Cys Val Thr Asp Glu Cys				
333 140 145 150				
335 cca att gct gtt ttc atg gtg gtg ttc cag tca atc gtg ggc tgc atc				893
336 Pro Ile Ala Val Phe Met Val Val Phe Gln Ser Ile Val Gly Cys Ile				
337 155 160 165 170				
339 atc gat gct ttc atc att ggc gca gtc atg gcc aag atg gca aag cca				941
340 Ile Asp Ala Phe Ile Ile Gly Ala Val Met Ala Lys Met Ala Lys Pro				
341 175 180 185				
343 aag aag aga aac gag act ctt gtc ttc agt cac aat gcc gtg att gcc				989
344 Lys Lys Arg Asn Glu Thr Leu Val Phe Ser His Asn Ala Val Ile Ala				
345 190 195 200				
347 atg aga gac ggc aag ctg tgt ttg atg tgg cga gtg ggc aat ctt cgg				1037
348 Met Arg Asp Gly Lys Leu Cys Leu Met Trp Arg Val Gly Asn Leu Arg				
349 205 210 215				
351 aaa agc cac ttg gtg gaa gct cat gtt cga gca cag ctc ctc aaa tcc				1085
352 Lys Ser His Leu Val Glu Ala His Val Arg Ala Gln Leu Leu Lys Ser				
353 220 225 230				
355 aga att act tct gaa ggg gag tat atc cct ctg gat caa ata gac atc				1133
356 Arg Ile Thr Ser Glu Gly Glu Tyr Ile Pro Leu Asp Gln Ile Asp Ile				
357 235 240 245 250				
359 aat gtt ggg ttt gac agt gga atc gat cgt ata ttt ctg gtg tcc cca				1181
360 Asn Val Gly Phe Asp Ser Gly Ile Asp Arg Ile Phe Leu Val Ser Pro				
361 255 260 265				
363 atc act ata gtc cat gaa ata gat gaa gac agt cct tta tat gat ttg				1229
364 Ile Thr Ile Val His Glu Ile Asp Glu Asp Ser Pro Leu Tyr Asp Leu				
365 270 275 280				
367 agt aaa cag gac att gac aac gca gac ttt gaa atc gtg gtc ata ctg				1277
368 Ser Lys Gln Asp Ile Asp Asn Ala Asp Phe Glu Ile Val Val Ile Leu				
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/591,628

DATE: 09/13/2006

TIME: 11:11:48

Input Set : A:\A0852.70000US01 seq.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number